

SEQUENCE LISTING

<110> ZENECA LIMITED

<120> GST SEQUENCES FROM SOYBEAN AND THEIR USE IN THE
PRODUCTION OF HERBICIDE RESISTANT PLANTS

<130> ZENECA CASE PPD50449/WO

<140>

<141>

<150> GB9922346.3

<151> 1999-09-21

<160> 43

<170> PatentIn Ver. 2.0

<210> 1

<211> 499

<212> PRT

<213> Glycine max

<400> 1

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Arg	Ile	Asp	Gln	Lys	Leu	Leu	Gln	Asn	Ile	Val	Tyr	Asp	Ala	Leu	Val
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Trp	Ser	Thr	Leu	Asn	Cys	Leu	Leu	Val	Gly	Asp	Lys	Ser	Val	Gln	Arg
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- 2 -

Ala Pro Ile Phe Asn Glu Leu Val Asp Arg Val Ser Leu Asp Gly Lys
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Phe Leu Gln Glu Ser Leu Ser Arg Thr Lys Asn Ala Asp Glu Phe Thr
 115 120 125

Ser Arg Leu Leu Asp Ile His Ser Lys Met Leu Gln Ile Asn Lys Lys
 130 135 140

Glu Asp Ile Arg Met Gly Ile Val Arg Ser Asp Tyr Met Ile Asp Glu
 145 150 155 160

Lys Thr Lys Ser Leu Leu Gln Ile Glu Met Asn Thr Ile Ser Thr Ser
 165 170 175

Phe Ala Leu Ile Gly Cys Leu Met Thr Gly Leu His Lys Ser Leu Leu
 180 185 190

Ser Gln Tyr Gly Lys Phe Leu Gly Leu Asn Ser Asn Arg Val Pro Ala
 195 200 205

Asn Asn Ala Val Asp Gln Ser Ala Glu Ala Leu Ala Lys Ala Trp Ser
 210 215 220

Glu Tyr Asn Asn Pro Arg Ala Ala Ile Leu Val Val Val Gln Val Glu
 225 230 235 240

Glu Arg Asn Met Tyr Glu Gln His Tyr Ile Ser Ala Leu Leu Arg Glu
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Lys His His Ile Arg Ser Ile Arg Lys Thr Leu Thr Glu Ile Asp Gln
 260 265 270

Glu Gly Lys Ile Leu Pro Asp Gly Thr Leu Ser Val Asp Gly Gln Ala
 275 280 285

Ile Ser Val Val Tyr Phe Arg Ala Gly Tyr Thr Pro Lys Asp Tyr Pro
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Ser Glu Ser Glu Trp Arg Ala Arg Leu Leu Met Glu Gln Ser Ser Ala
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Ile Lys Cys Pro Thr Ile Ser Tyr His Leu Val Gly Thr Lys Lys Ile

- 3 -

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Leu Glu Asp Ser Asp Ile Val Lys Lys Ala Ile Glu Asn Pro Glu Leu		
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Phe Val Met Lys Pro Gln Arg Glu Gly Gly Gly Asn Asn Ile Tyr Gly		
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Asp Glu Leu Arg Glu Thr Leu Leu Lys Leu Gln Glu Ala Gly Ser Gln		
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Glu Asp Ala Ala Tyr Ile Leu Met Gln Arg Ile Phe Pro Ala Thr Ser		
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Pro Ala Ile Leu Val Arg Asp Gly Asn Trp Asp Thr Gly His Val Ile		
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Ser Glu Ala Gly Ile Phe Gly Thr Tyr Leu Arg Asn Lys Asp Lys Ile		
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<213> Artificial Sequence

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<223> Description of Artificial Sequence:Protein

- 4 -

Fragment

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:Protein
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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Protein
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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Protein
Fragment

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<210> 6

<211> 1854

<212> DNA

<213> Glycine max

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<212> PRT

<213> Glycine max

<400> 7

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Tyr Lys Tyr Leu Glu Asp Asp Leu Asn Asn Lys Ser Asp Leu Leu Leu
 35 40 45

Lys Tyr Asn Pro Val Tyr Lys Met Ile Pro Val Leu Val His Asn Glu
 50 55 60

Lys Pro Ile Ser Glu Ser Leu Val Ile Val Glu Tyr Ile Asp Asp Thr
 65 70 75 80

Trp Lys Asn Asn Pro Ile Leu Pro Ser Asp Pro Tyr Gln Arg Ala Leu
 85 90 95

Ala Arg Phe Trp Ala Lys Phe Ile Asp Asp Lys Cys Val Val Pro Ala
 100 105 110

Trp Lys Ser Ala Phe Met Thr Asp Glu Lys Glu Lys Glu Lys Ala Lys
 115 120 125

Glu Glu Leu Phe Glu Ala Leu Ser Phe Leu Glu Asn Glu Leu Lys Gly
 130 135 140

Lys Phe Phe Gly Gly Glu Glu Phe Gly Phe Val Asp Ile Ala Ala Val
 145 150 155 160

Leu Ile Pro Ile Ile Gln Glu Ile Ala Gly Leu Gln Leu Phe Thr Ser
 165 170 175

Glu Lys Phe Pro Lys Leu Ser Lys Trp Ser Gln Asp Phe His Asn His
 180 185 190

- 7 -

Pro Val Val Asn Glu Val M t Pro Pro Lys Asp Gln Leu Phe Ala Tyr
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Phe Lys Ala Arg Ala Gln Ser Phe Val Ala Lys Arg Lys Asn
 210 215 220

<210> 8

<211> 235

<212> PRT

<213> Glycine max

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 20 25 30

Glu Tyr Val Glu Glu Asp Leu Arg Asn Lys Ser Asp Leu Leu Leu Lys
 35 40 45

Tyr Asn Pro Val His Lys Lys Val Pro Val Leu Val His Asn Gly Lys
 50 55 60

Ala Ile Ala Glu Ser Met Val Ile Leu Glu Tyr Ile Asp Glu Thr Trp
 65 70 75 80

Lys Asp Gly Pro Lys Leu Leu Pro Ser Asp Ser Tyr Lys Arg Ala Gln
 85 90 95

Ala Arg Phe Trp Cys His Phe Ile Gln Asp Gln Leu Met Glu Ser Thr
 100 105 110

Phe Leu Val Val Lys Thr Asp Gly Glu Ala Gln Gln Lys Ala Ile Asp
 115 120 125

His Val Tyr Glu Lys Leu Lys Val Leu Glu Asp Gly Met Lys Thr Tyr
 130 135 140

Leu Gly Glu Gly Asn Ala Ile Ile Ser Gly Val Glu Asn Asn Phe Gly
 145 150 155 160

- 8 -

Ile Leu Asp Ile Val Phe Cys Ala Leu Tyr Gly Ala Tyr Lys Ala His
 165 170 175

Glu Glu Val Ile Gly Leu Lys Phe Ile Val Pro Glu Lys Phe Pro Val
 180 185 190

Leu Phe Ser Trp Leu Met Ala Ile Ala Glu Val Glu Ala Val Lys Ile
 195 200 205

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 210 215 220

Leu Ser Ala Leu Lys Ser Ser Ser Ala Thr Glu
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<210> 9

<211> 223

<212> PRT

<213> Glycine max

<400> 9

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 20 25 30

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 35 40 45

Val Tyr Lys Lys Thr Pro Val Leu Val His Asn Gly Lys Pro Leu Cys
 50 55 60

Glu Ser Met Leu Ile Val Glu Tyr Ile Asp Glu Ile Trp Ala His Asn
 65 70 75 80

Ser Leu Leu Pro Ala Asp Pro Tyr Glu Arg Ala Leu Ala Arg Phe Trp
 85 90 95

Val Lys Tyr Ala Asp Asp Asp Met Phe Ser Ala Val Ile Ala Phe Phe
 100 105 110

- 9 -

Leu Ser Asn Asn Asp Glu Glu Arg Glu Lys Ser Ile Glu Lys Ile Trp
 115 120 125

Glu His Leu Arg Val Val Glu Asn Gln Cys Phe Gly Asp Gln Lys Lys
 130 135 140

Phe Phe Gly Gly Asp Ile Ile Asn Ile Met Asp Ile Ala Phe Gly Ser
 145 150 155 160

Ile Phe Lys Ile Leu Val Val Ala Glu Asp Ile Leu Asp Ala Lys Val
 165 170 175

Leu Glu Asp Glu Lys Phe Pro His Leu His Ser Trp Tyr Asn Asn Phe
 180 185 190

Lys Asp Val Ala Val Ile Lys Glu Asn Leu Pro Asp His Glu Lys Met
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Val Ala Phe Ala Lys Phe Ile Arg Glu Lys Arg Leu Ala Cys Thr
 210 215 220

<210> 10

<211> 232

<212> PRT

<213> Glycine max

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Val Val Glu Glu Thr Leu Asn Pro Lys Ser Glu Leu Leu Leu Lys Ser
 35 40 45

Asn Pro Val His Lys Lys Ile Pro Val Phe Phe His Gly Asp Lys Val
 50 55 60

Ile Cys Glu Ser Ala Ile Ile Val Glu Tyr Ile Asp Glu Val Trp Ser
 65 70 75 80

- 10 -

Asn Asn Ala Leu Ser Ile Leu Pro Gln Asn Ala Tyr Asp Arg Ala Asn
 85 90 95

Ala Arg Phe Trp Val Ser Tyr Ile Asp Asp Lys Trp Leu Thr Ser Leu
 100 105 110

Lys Ser Val Leu Ala Thr Glu Asp Asp Glu Ala Lys Lys Leu His Phe
 115 120 125

Glu Gln Ala Glu Glu Val Leu Glu Lys Val Glu Glu Val Phe Asn Lys
 130 135 140

Cys Ser Glu Gly Lys Ala Tyr Phe Gly Gly Asp Thr Ile Gly Phe Val
 145 150 155 160

Asp Ile Gly Phe Gly Ser Phe Leu Ser Phe Ile Arg Val Ser Glu Asn
 165 170 175

Met Asn Glu Arg Lys Leu Leu Asp Glu Thr Lys Tyr Pro Gly Leu Thr
 180 185 190

Leu Trp Ala Glu Thr Phe Ala Ala Asp Pro Ala Val Lys Gly Leu Leu
 195 200 205

Pro Glu Thr Glu Lys Leu Val Glu Phe Ala Lys Ile Leu Gln Leu Lys
 210 215 220

Trp Ala Ala Ala Ala Ala Lys
 225 230

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<211> 885

<212> DNA

<213> Glycine max

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- 11 -

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<211> 840

<212> DNA

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- 12 -

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<212> DNA

<213> Glycine max

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<223> Description of Artificial Sequence:PRIMER

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<210> 19

<211> 23

<212> DNA

<213> Artificial Sequence

- 14 -

<220>

<223> Description of Artificial Sequence:PRIMER

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:PRIMER

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<210> 21

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:PRIMER

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:PRIMER

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<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:PRIMER

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<210> 25

<211> 2763

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:SOYBEAN Derived
nucleic acid sequence P32110

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gca 2763

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<210> 26

<211> 1137

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Mungbean
Sequence U20809

<400> 26

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gttgaagaaa atttccgcaa caagagtgaag cagcttctga aatacaaccc agttcacaag 180
aagggtccag tgtttgttca tgggtgacaaa ccccttccag agtcccttgt gattgttgag 240
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<210> 27

<211> 2038

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Tobacco
sequence Q03663

<400> 27

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gaaagaagaa gacacaaact gtgtttggta ttattatagt tttttctttt agagaattga 420
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tcaaagtatt tatttttaaat tctttttcca atggacattc ccattctgaa aaaaaagaga 540
tataaatatg gaagtaaaaa ttaatcgat cgttaaatgt agaaaatatt aattaacaca 600
ttaaccataa ccagtcctact ttatttaaca aaagcacat ctgaratarc aaaaaagtg 660
ttaacttcat gcattgacaa tttaaaatta ttttgcaaca tcgggtaaaa ctattttaca 720

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<210> 28

<211> 2796

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Potato- Derived
nucleic acid sequence P32111

<400> 28

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aattacttat gcagttcttg aaccctttgt gagacgagag ggagttgctc ggatggtaag 240
cacccttcac tttcaacccg aagggtgcga gtttgagtca ccaacggagc aaaaagggta 300
ggagctccta gaaagggtaa aaaaaaaaaa aaaaattaat aaaaaatac cctttatgaa 360
atttctcatt ccgctactgc acttctcccc tgatcttctt cgtgttttca attattaatt 420
ctatattcat gacaccatgt gatgtttctc tgggtagtcc taaaaataga ggtattgaaa 480
attatgttgt ttctctctgg tctatttact tttcttgtgt actttattgt atttcatatt 540
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<210> 29

<211> 1289

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Arabidopsis

P46421

<400> 29

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aaaaggtagt gattaactcc acaaaaccag aaaaactaca tttctaacat atagaagaaa 300
cagagaaaaa gagagagaga cccctaattg ctgagaaaga agaagtgaag cttttgggga 360
tatgggagag cccttttagc cgctgggtcg agatggctct caaactcaaa ggcataaccgt 420
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gttgtgtggt tgagaagtga ggttttatca tcatctctca cgttatctta tttgggtcca 1260
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<210> 30

<211> 1339

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Arabidopsis

Genomic sequence

<400> 30

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agagataaaa aaaaattgta tagggaacgt tataaatatg ttgtaaagtc aacatctggt 180
tccttctaga ctcttcgcat ttacatcaca ctgccgacca tataaaacgg caaagttcgt 240
cgctgtttta tcacaagacc atcaacacca taaggctata aatccaagct aaaaggtagt 300

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gattaactcc acaaaaccag aaaaactaca tttctaacat atagaagaaa cagagaaaaa 360
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cccttttagc cgtcgggtcg agatggctct caaactcaaa ggcataccgt acgagtacgt 480
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caatgtttgt atggttatgt tgttgtttat tttattgaat atctttgtat gttgtgtggt 1260
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agaattaatg gtaaagctt                                     1339

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<210> 31

<211> 968

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Papaya AJ000923

<400> 31

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tggaatgaga atcagaatcg ctttagccga gaagggtatt cactacgagt acaaggaaga 180
gaatctgaga aacaagagtc cttactcct gcagatgaac ccggtacaca agaaaatccc 240
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tgtgtgtgacg tcaattttctt gtgtgttgta ggcaaatcat atttgaataa aatctttctt 960
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<210> 32

<211> 1040

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Spruce AF051214

<400> 32

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<210> 33

<211> 902

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Wheat AF004358

<400> 33

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aactgacac acatcgatcg aggtagttag agatggccgg aggagatgac ctgaagctgc 120
tcggcgcatg gccaaagcca tttgttacca ggggtgaagc ggcgctcgcc ctgaagggcc 180

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tgagctacga ggacgtggag gaggacctgt acaagaagag tgagcttctc ctcaagtcca 240
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tgatcattct ccagtacatc gacgaagtgt tcgccagcac cgccccgtcc cttcttccag 360
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<210> 34

<211> 1127

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Spruce AF051238

<400> 34

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<211> 34

<212> DNA

<213> Artificial Sequence

<220>

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34

<210> 36

<211> 234

<212> PRT

<213> Glycine max

<400> 36

Met Ser Lys Ser Glu Asp Leu Lys Leu Leu Gly Gly Trp Phe Ser Pro

1

5

10

15

Phe Ala Leu Arg Val Gln Ile Ala Leu Asn Leu Lys Gly Leu Glu Tyr

20

25

30

Glu Val Val Glu Glu Thr Leu Asn Pro Lys Ser Asp Leu Leu Leu Lys

35

40

45

Ser Asn Pro Val His Lys Lys Ile Pro Val Phe Phe His Gly Asp Lys

50

55

60

Val Ile Cys Glu Ser Ala Ile Ile Val Glu Tyr Ile Asp Glu Ala Trp

65

70

75

80

Thr Asn Val Pro Ser Ile Leu Pro Gln Asn Ala Tyr Asp Arg Ala Asn

85

90

95

Ala Arg Phe Trp Phe Ala Tyr Ile Asp Glu Lys Trp Phe Thr Ser Leu

100

105

110

Arg Ser Val Leu Val Ala Glu Asp Asp Glu Ala Lys Lys Pro His Phe

115

120

125

Glu Gln Ala Glu Glu Gly Leu Glu Arg Leu Glu Glu Val Phe Asn Lys

130

135

140

- 25 -

Tyr Ser Glu Gly Lys Ala Tyr Phe Gly Gly Asp Ser Ile Gly Phe Ile
 145 150 155 160

Asp Ile Gly Phe Gly Ser Phe Leu Ser Trp Met Arg Val Ile Glu Glu
 165 170 175

Met Ser Gly Arg Lys Leu Leu Asp Glu Lys Lys His Pro Gly Leu Thr
 180 185 190

Gln Trp Ala Glu Thr Phe Ala Ala Asp Pro Ala Val Lys Gly Ile Leu
 195 200 205

Pro Glu Thr Asp Lys Leu Val Glu Phe Ala Lys Ile Leu Gln Leu Lys
 210 215 220

Trp Thr Ala Ala Ala Ala Ala Ala Lys
 225 230

<210> 37

<211> 222

<212> PRT

<213> Glycine max

<400> 37

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Pro Phe Leu His Arg Val Gln Ile Ala Leu Lys Leu Lys Gly Val Glu
 20 25 30

Tyr Lys Tyr Leu Glu Asp Asp Leu Asn Asn Lys Ser Asp Leu Leu Leu
 35 40 45

Lys Tyr Asn Pro Val Tyr Lys Met Ile Pro Val Leu Val His Asn Glu
 50 55 60

Lys Pro Ile Ser Glu Ser Leu Val Ile Val Glu Tyr Ile Asp Asp Thr
 65 70 75 80

Trp Lys Asn Asn Pro Ile Leu Pro Ser Asp Pro Tyr Gln Arg Ala Leu
 85 90 95

- 26 -

Ala Arg Phe Trp Ala Lys Phe Ile Asp Asp Lys Cys Val Val Pro Ala
 100 105 110

Trp Lys Ser Ala Phe Met Thr Asp Glu Lys Glu Lys Glu Lys Ala Lys
 115 120 125

Glu Glu Leu Phe Glu Ala Leu Ser Phe Leu Glu Asn Glu Leu Lys Gly
 130 135 140

Lys Phe Phe Gly Gly Glu Glu Phe Gly Phe Val Asp Ile Ala Ala Val
 145 150 155 160

Leu Ile Pro Ile Ile Gln Glu Ile Ala Gly Leu Gln Leu Phe Thr Ser
 165 170 175

Glu Lys Phe Pro Lys Leu Ser Lys Trp Ser Gln Asp Phe His Asn His
 180 185 190

Pro Val Val Asn Glu Val Met Pro Pro Lys Asp Gln Leu Phe Ala Tyr
 195 200 205

Phe Lys Ala Arg Ala Gln Ser Phe Val Ala Lys Arg Lys Asn
 210 215 220

<210> 38

<211> 895

<212> DNA

<213> Glycine max

<400> 38

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 gtctagaata tgaggttggt gaagagacct tgaatcccaa aagtgacctg cttcttaagt 180
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 gttggatgag agtcatagag gagatgagtg gaagaaaatt gcttgatgaa aagaagcacc 600
 ctggtttgac ccaatgggct gaaacgtttg ctgctgatcc tgctgtgaag ggcattcttc 660

- 27 -

cagagactga taagcttggt gagtttgcca agattcttca gctaaaatgg actgctgcag 720
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 gtccaagttg tttttatctc aggctatggt gttgcaactt tatttattta aaagttattt 840
 taaatttaaa atgtaaaata ttaagaaagt ttaagtaagt tagttgaaaa atttt 895

<210> 39

<211> 895

<212> DNA

<213> Glycine max

<400> 39

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 agattgctct caagttgaag ggagttgaat acaaattttt ggaagacgat ttgaacaaca 180
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 ctaaattggag ccaagacttt cacaaccatc cagttgtcaa cgaagttatg cctcctaagg 660
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 aatatagtga gactcagaat ttccatcgag gtttcagtat tgtatgaaat gaaagctact 780
 tgtctatggt tcgttattgc ggttgatatt tcatttttca atgaattatg tgatatagga 840
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<210> 40

<211> 977

<212> DNA

<213> Glycine max

<400> 40

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 gaagcttttg ggagctactg gaagcccatt tgtgtgcagg gttcagattg cctcaagtt 180
 gaagggagtt caatacaaat ttttggaaga aaatttgagg aacaagagtg aactgcttct 240
 caaatccaac ccagttcaca agaaggttcc agtgtttatt cacaatgaga agcccatagc 300
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 tgtgggtgct gcatggaaat atattttatac tggtgatgag aaagagcgtg agaagaatgt 480
 tgaagagtca tatgaggctc tgcagtttct tgagaatgag ctgaaggaca agaagttttt 540
 tggaggagag gaaattgggt tggtagatat tgctgctgct tcatagcat tttggatccc 600

- 28 -

tatatttcaa gaagtattgg gtttgaagtt attcacaagt gagaaatttc ctaagctcta 660
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<210> 41

<211> 1006

<212> DNA

<213> Glycine max

<400> 41

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 aagaaaattt gaggaacaag agtgaactgc ttctcaaacc caaccagtt cacaagaagg 180
 ttccagtgtt tattcacaat gagaagccca tagcagagtc tcttgtgatt gttgaatata 240
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 tcttgagaat gagataaagg acaagaagtt ctttgaggga gaggagattg ggttggtaga 480
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 gttattcaca agtgagaaat ttcctaagct ccacaattgg agccaagaat ttttgaacca 600
 tccaattgtc aaagaaagtc tgccccctag agatcctggt ttctcctttt tcaagggctc 660
 ctatgaaagc ctttttggtt caaaatagat ttgatgatgt ggtgtgagac ttagtatttc 720
 taagaattat gtgtttgtta aaggcttcta tgaaagcctc actgcttcaa aatagattca 780
 tgtatgtgag actcagaatc tctggggaaa attgtgtgtg gtgtggacta cttgttttgt 840
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 aataaatata tagcatcttt ctatttctca aaaaaaaaaa aaaaaa 1006

<210> 42

<211> 885

<212> DNA

<213> Glycine max

<400> 42

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 tacttgttca taatggaaag gccattgctg aatccatggt gatccttgag tatattgatg 240
 aaacatggaa agatggtcct aaactgcttc caagtgattc ttacaaacga gcccaagctc 300

- 29 -

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 tacttcaaca ctttaataga ctgtccatcg tttgttctt ctgcgagtct ttagtgtatg 780
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<210> 43

<211> 991

<212> DNA

<213> Artificial Sequence

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 aagaagaagt gaggtctattg ggcaagtggg ccagcccatt tagcaacaga gtagaccttg 180
 ctctcaagct caaggggtgtt cctacaaat actccgagga agatcttgct aacaagagtg 240
 ctgatcttct caagtacaac cccgttcaca agaaggttcc ggtttttggtc cacaatggga 300
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 cactattgcc tcaagacca tatgaaagag ccttggtctg tttttggtct aagaccttag 420
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 agttatataa ttggagtcaa gactttatca accaccctgt gatcaaggag ggtctgcctc 720
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991